

FIG.1

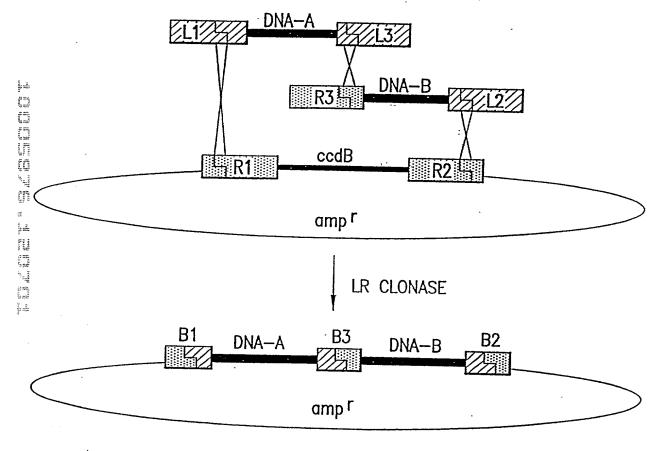


FIG.2

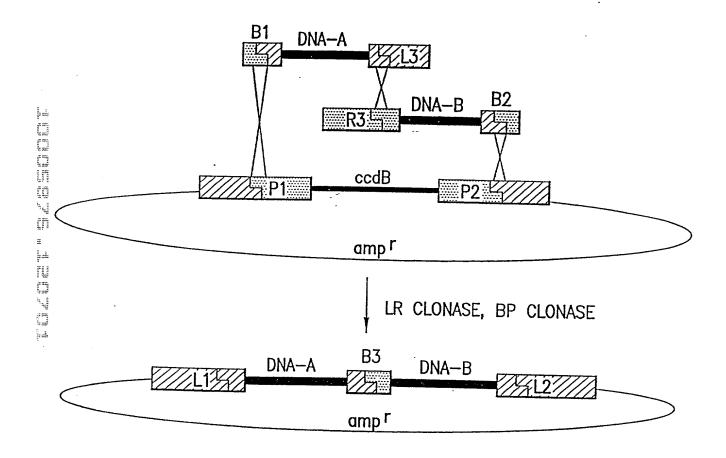


FIG.3

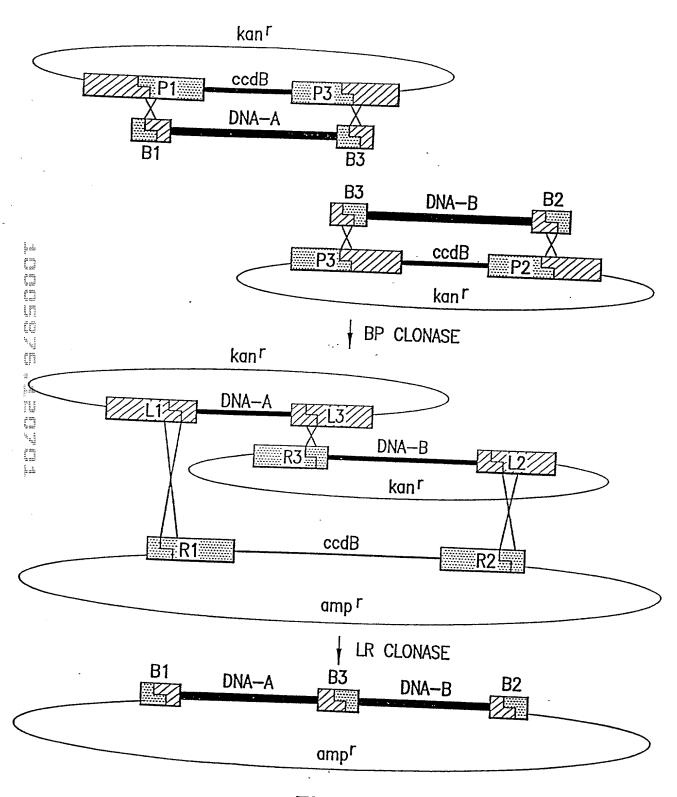


FIG.4

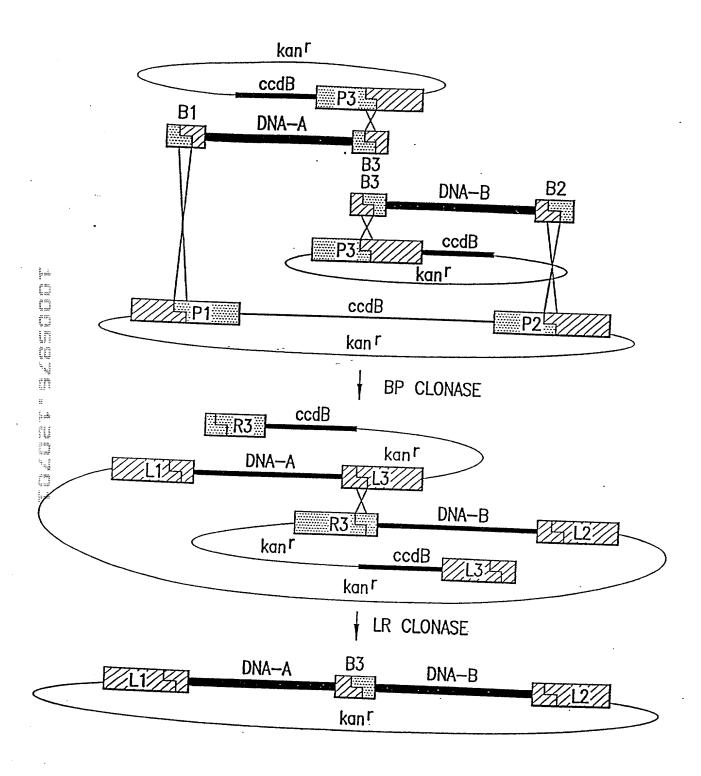


FIG.5

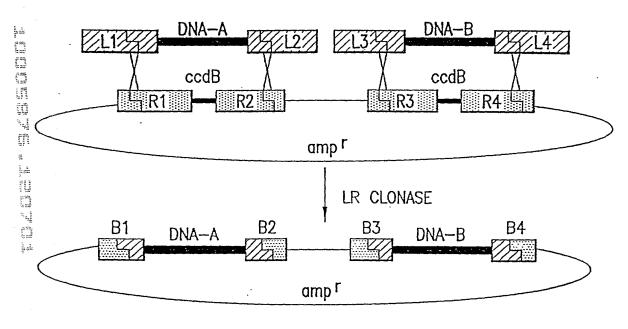


FIG.6

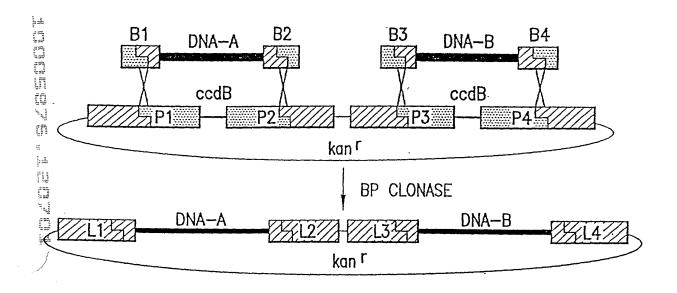


FIG.7

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	GGAACAAGGG
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	——— GGGAACCGGAT	53			ccctrggccta	gggaaccggaT					GGGAACCGGAT
GENE OF INTEREST			PCR	- ->				+ TOPO	>		
					CGGAACAAGGG	GCCTTGTTCCC				CGGAACAAGGG	TTCCC

FIGURE 8A

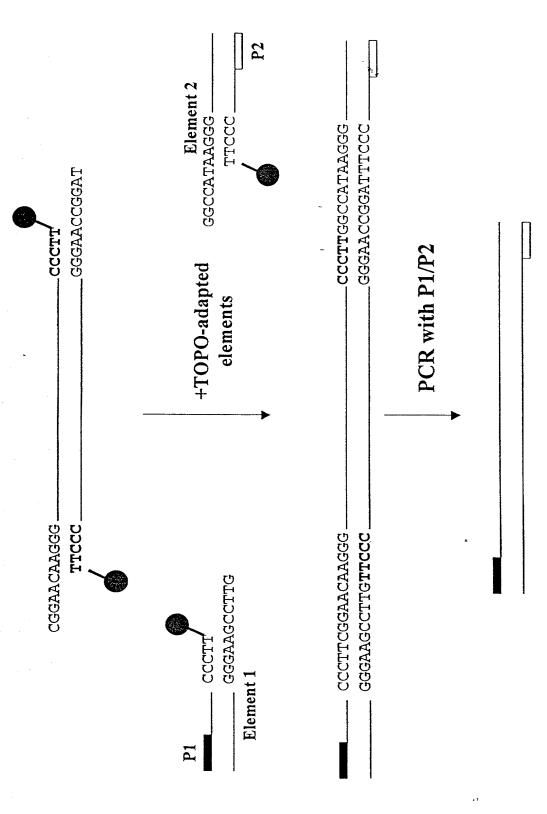


FIGURE 8B

BGH element (32) F7222 GGCCAAGGG T7C22 TTCCC F6948	(36) GGCCAAGGG TTCCC	GGCCTAAAGGG F8419 TTCCC F6948
GFP element (30) F7220 TCGAAAGGG ——CCCTT TTCCC ——F6682 — GGGAACCGG (31)	CGGAACAAGGG F8418 CGGAACAAGGG CCCTT TTCCC F6682 GGGAACCGG (35)	CGGAACAAGGG F8418 TTCCC F8420 GGGAACCGGAT (39)
CMV element A:. F6945 CCCTT F7221 GGGAA AGCT (29)	B. F6945 CCCTT F8417 GGGAA GCCTTG R333	C. F6945 CCCTT F8417 GGGAA GCCTTG (37)

France 94-C

TATGECTATOCTACCATACGATTTAGGT	Primer name F#	世里	Spainages 51, 5, 21	_
10780 ACCECTIOTORINGON ACCECTIOTORINGON ACCECTIOTOCCCCCCCCTION ACCECTIOTOCCCCCCCTION ACCECTION ACCETION ACCECTION ACCETION	MTH1	10779	TATGTATCATACACATTCACCT	SEQ ID NO:
12667 GTTCCGAAGGGGATATCAGAAGTTCTGTCTTTG 12668 ITGCCCAAGGGGTATCTAGAAGCTTCTGCAGAGGGGT 12668 GTTCCGAAGGGCTACTCGTCAATTCCAGGT 12668 GTTCCGAAGGGCTACTCGTCAATTCCAGGTTATTAGGGGTACTTGTATTGCAGGTTATTAGGGGTACTGGAATTCCAGGTTATTAGGGTTGAATTGCAGGTTATTGCAGGTTGAATTGCAGGTTGAATTGCAGGTTGAATTGCAGGTTGAATTGCAGGTTGAATTGCAGGGAATTCCGGGGAATTGCGGGAATTGCGGGAATTGCGGGAATTGCGGGAATTGCGGGAATTGCGGGAATTGCGGGAATTGCGGGAAGGGTTGAATTGCGAAGGGTTGAATTGCGAAGGGTTGAATTGCGCAAGGGTTGAATTGCGCAAGGGTTGAATGGGGCAAGGGTTGAATGGGGCAAGGGTTGAATGGGGCAAGGGAAGGGTTGAATGGGGCAAGGGGTTGAATGGGGCAAGGGGTTGAATGGGGCAAGGGGTTGATGAAGGGTCGAAGGGTTGGAAGGGGTTGAATGGGGCAAGGGGTTGATGGGGGAAGGGTTGATGGGGCAAGGGGTTGAATGGGGCCAAGGGGTTGGTGGGGGAAGGGTTGGAATGGGGCCAAGGGGTTGGAAGGGGTTGAATGGGGCCAAGGGGTTGATGGGGCAAGGGGTTATAGGGCCAAGGGGTTATAGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAATAAGGGGTTAAAGGGGCCAATAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAATAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGGCCAAGGGCCAAGGGCCAAGGGCCCAAGGGCCCAAGGGGCCAAGGGCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCAAGGCCAAGGCCCAAGGCCCAAGGCCCAAGGCCAAGGCCAAGCCAAGCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAAAGA	MTH2	10780	ACCECTOTOCOCACATT	
12505 TTGGCCAAGGGTATCTAGAAGGTTOTGCAGGGGT 12868 GTTCCGAAGGGCTACTCGTCAATTCCAGGGGT 12868 GTTCCGAAGGGCCACCGGTACTCGTCAATTCCAGGGTTATTAATGCAGGTTATTAATGCAGGGTTATTAATGCAGGTTATTAATGCAGGTTATTAATGCAGGTTATTAATGCAGGTTATTAATGCAGGTTATTAATGCAGGTTATTAATGCAGGTTGCAGGTTGGAATTCCGGGGGAATTCCCGGGGGATTTGCAGGTTGGAATTCCGGGGGAATTCCGGGGGAATTCCGGGGGAATTCCGGGGGAATTCCGGGGGAATTCCGGGGGAATTCCGGGGGAATTCCGGGGGAAGGGTTAATTAA	GAL412	12667	GTTCCGAAGGGGGATACAACTCAACTTTC	2
2 12668 GTTCCGAAGGGCCACCGTACTCGTCAGTTCAGGG 24 12016 GGCCAAAAGGGAACTTGTTATTCCAGCTTATATGC 24 561 CTCTGACTTGAGCGTCGATTTT 12669 CGGAACAAGGGGAATTCCCGGGGACTC 12670 CGGAACAAGGGGAATTCCCGGGGATTC 12670 CGGAACAAGGGGAATTCCCGGGGATTC 12671 TCGAAAGGGGAATTCCCGGGGATTC 12672 TCGAAAGGGTCGACTGCACTGCAGTG 12721 TCGAAAGGGTTGTAGGTAA 12722 GCCCAAGGGTTGTAGGCCCGCATAGT 12722 GCCCAAGGGTTGAATGGGCCCGCATAGT 12823 GGCCAAGGGTTTGTAGAGCCCGCATAGT 128248 AAGCCATAGAGCCCAGCAAAGGAGAAG 12848 AAGCCATAGAGCCCAGCAAAGGAGAAG 12848 AAGCCATAGAGCCCAGCAAAGGAGAAG 12848 AAGCCAAAGGGTTTGTAGGCCCCATAGT 12848 AAGCCAAAGGGTTGAATGGGCCCCATAGT 12849 GCCCTAAAGGGTTAAGGGCCCCATAGT 12840 GACCCAAGGGTTTAAGGGCCCCATAGT 12841 GACCCAAGGGTTAAAGGGGCCCATAGT 12852 GCGCAAGGGTTAAAGGGGCCATAAGGGGCCCATAAGGGGCCCATTAAGGGCCCATTAAGGGGCCCATTAAGGGGCCCATTAAGGGGCCCATTAAGGGGCCCATAAGGGGACCATTAAGGGCCCCATAAGGGGACCATTAAGGGCCCATAAGGGGACCATTAAGGGCCCATAAGGGGCCCATAAGGGGCCCATAAGGGGC	MTH5	12505	TTGGCCAAGGTATCTAGAAGCTTCTGCAGACGCT	ന
12016 GGCCAAAAGGGAACTTGTTTATTGCAGCTTATAATG 12689 CTCTGACTTGAGCGTCGATTTT 12689 CGGAACAAGGGGAATTCCCTGTCAGCGTGAGATTC 12870 CGGAACAAGGGGAATTCCCTGTCAGCTG 1221 TCGAAAGGGGAATTCCCTGCAGCTG 1221 TCGAAAGGGTCAACTGCCTGCAGCTG 1221 TCGAAAGGGTCAATTGCCCAGCAAGGAAG 1222 GGCCAAGGGTTTATTGAGCCAGCAAGGAAG 1222 GGCCAAGGGTTTATTGAATGGGCCCAGTAGT 1222 GGCCAAGGGTTTGAATGGGCCCAGTAGT 1222 GGCCAAGGGTTTGAATGGGCCCATAGT 1222 GGCCAAGGGTTTGAATGGGCCCATAGT 1224 GGCCAAGGGTTTGAAGGTCCAGCTGC 1224 GGCCAAGGGTTTGAAGGTCCAAGGGCTCATAGT 1225 GGCCAAGGGTTTGAAGGTCCAAGGGCTCATAGT 1226 GGCCTAAAGGGTTTGAAGGTCCATAGT 1226 GACCAAAGGGTTTGAAGGTCCATAGT 1226 GACCAAAGGGTTTGAAGGTCCATAGT 1226 GACCAAAGGGTTTGAAGTCCATAGT 1226 GACCAAAGGGTTTGAATTGCGCCATAGT 1226 GACCAAAGGGTTTAATACCCTTCATAGTGGGCCCATAGT 1226 GACCAAAGGGTCCATTAAGGGGTTAATTGCGCCCTTAAGTGGGCCCATAGT 1226 GACCAAAGGGTCCATTAAGGGGTTAATTGCGCCTTAAGTGGGCTTAATTGGCCCTTAAGGGGTTAATTGGCCCTTAAGGGGTTAATTGCGCTTAAGGGGTTAATTGCGCCTTAAGGGGTTAATTGCGCCTTAAGGTCCCTTAAGGGGTTAATTGCGCCTTAAGGGGTTAATTGCGCCTTAAGGGGTTAATTGCGCCTTAAGGGGTTAATTGCGCCTTAAGGGGTTAATTGCGCCTTAAGGGGGTTAATTGCGCCTTAAGGGGTTAATTTAATTGCGCCTTAAGGTCCTTTAAGTTCCGCTTATAGTTCCGACTTTAAGTTCCCAAGGGGATGATTTACATCCCTTCATTAAGGGGATGATTAAGATCCGCTTAAGGTCCATTAAGATCCCTTCATTAAGGTCCATTAAGATCCCATAGTTTAAGATCCCATAGGTTTAAGATCCCATAAGGGGATGATTAAGATCCCATAGGTTTAAAGGTTTAAAGGTTTAAGATCCCATAGGTTTAAAGGTTTAAGATCCCATAAGGTTTAAAGGTTTAAGATCCCATAGGTTTAAAGATCCCATAAGGTTTAAAGGGATGATTAAGATCCCATAGGTTTAAAGATCCCATAAGGTTTAAAGGTTAAAAGGTTAAAAGGTTAAAAGGTTAAAAGGTTAAAAGGTTAAAAGGTTAAAAGAAAGAAAAAA	VP16r2	12668	GTTCCGAAGGGCCACCGTACTCCAATTCCAAG	77
12670 12670 12689	SV40pAf	12018	GGCCAAAAGGGAACTTGTTATTGCAGCTTATAATA	1 /1
12669 CGGAACAAGGGGAATTCCCTGTCAGCGACCC 12670 CGGAACAAGGGGGAATTCCCGGGGGATTCC 12670 CGGAACAGGGGGAATTCCCGGGGGATTCCGGTGGAATTCCGGGGGAATTCCGAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCGTGAGTAGTA TCGAAAGGGGTAATGGGCCAGCAAGGGAAGGAGAGGAAGGGGTTTGTAGAGCCCGGGCCAAGGGCTTGAATGGGCCCGCATAGT 6848 AAGCCATAGAGCCCGGGCCAAGGGCTCATCCATGGCCCAAGGGGTTGAATGGGCCCAAGGGTTGAGAGCTCATGGGCCCAAGGGGTTGATAGTGGGCCCATAGT 8418 CGGCAACAAGGGTTGATAGTCCATGGGCCCATAGT CGGAACAAGGGGTTGATAGGGGCCCCATAGTGGGGCCCATAGT 1418 CGGCAACAAGGGGTTGATAGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTGATAGTGGGGCCCATAGTGGGGCCCATAGTGGGGCCCATAGTTAATTGGGCCCATAGTGGGGCCCATTAGTGGGGCCCATTAGTGGGGCCCATTAGTGGGGCCCATTAGTGGGGCCCATTAGTGGGGCCCTTAGGGCCCTTTAGGCCCATGGTGATTAGTGGGGCCCATTAGTGGGGCCCATTAGTGGGGCCCTTAGGCGCCCTTTAGGCCCTTTAGGCCCTTTAGGCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCTTTAGGCCCTTTAGGCCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCCTTTAGGCCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCTTTAGGCCCCCCTTTAGGCCCCCCTTTAGGCCCCCCTTTAGGCCCCCCCC	SV40pAr	561	CTCTGACTTGAGCGTCGATTTT	9
12870 CGGAACAAGGGAATTCCCGGGGATTTGAATTC	p53f2	12669	CGGAACAAGGGGAATTCCCTGTCACCGAGACC	~
7221 TCGAAAGGGTCGAGGTCGACGTGCGTTTTTTTTTTTTTT	SVTr2	112670	CGGAACAAGGGGAATTCCCGGGGATCTGGAATTC	m)
10772 17220 17220 17220 17220 17220 17220 17220 17220 17220 17220 17220 17220 17220 17220 17220 17222 17222 17222 17222 17222 17222 17222 17220 17222 17222 17222 17222 17222 17222 17222 17220 17222 17222 17222 17222 172220 17222 172220 172220 17222 172220 17222 172220 1722	CMVZ	7221	TOGAAAGGGTCGAGCTGCAGCTG	Δ'n
17220 TCGAAAGGGTAATEGCCAGGAAAGGAGAAG 17220 GGCCAAGGGTTTGTAGAGGTCATCCAT 17222 GGCCAAGGGTTTGTAGAGGTCATCCAT 18418 AAGCCATAGAGGTCAGCCACAGGGTG 18418 GGCCAAGGGTCGAGCAAAGGGCTG 18418 GGCCAAGGGTTGTAGAGGTCATCCATGC 18418 GGCCAAGGGTTTGTAGAGGTCATCCATGC 18419 GGCCTAAAGGGTTAATGGGCCCCATAGT 18304 GAAGGAGTAATACGACTCATAGT 18306 GAAGGAGTAATACGACTCATTAGGGCCCATAGTCATTAGTCGCCCATAGTCATAGTCATTAGTC	CMVf	6945	AATTCACATTGATTATTGAGTAGTTA	10
off 6682 GGCCAAGGGTTTGTAGAGCTCATCCAT 7222 GGCCAAGGGTCTGAATGGGCCCGATAGT 6848 AAGCCATAGAGCCCGGCCCA 8417 GTTCCGAAGGGTCGACCTGCACCTGCAGCTG 8418 CGGAACAAGGGTTGCCATCATCCATGC 8419 GGCCTAAAGGGTTGAATGGGGCCCATAGT 9304 GAAGGAGTAATACGACTATAGGGCCCATAGT 9305 GAAGGAGTAATACGACTCACTATAGGGAGCCACCATGGTATTACTCCTTC 9861 GAAGGAGTAATACGACTCACT 9861 GAAGGAGTAATACGACTCACT 9862 GCCCTAAAGGGTCATTAGTGAGGTTAATTGCGCC 1066 GCCTAAAGGGTCATTAGTGAGTTAATTGCGCC 1067 TAGGCCAATTAACGACTCACTTAAAGGGGTTTAATTGCGCC 1066 GCGCGAATTAACGACTCACTTAATGCGCTTTTAGTAATTGCGCC 1067 TAGGCCAAGGGGATTTTCAATCCGCTTTTACTCCTTTTAATTGCGCCTTTAGTAATTGCGCAACTTCACCTTTAATTTACAATCCCGTTTTACAATCCCGTTTTACAATCCCGTTTTACAATCCCGTTTTACAATCCCCTTTAATTACAATCCCCTTTTAATTACAATCCCCTTTTAATTACAATCCCAACTGCTTTTACAATCCCCTTTCCAATTATTACAATCCCAACTGCTTTTAATTACAATCCCAAACTGCTTTAATACAAGGGGTTTTAAATTACAAGGGATTTTTACAATCCCAACTGCTTTAATACAAGGGTTTAAATCCCAAACTGCTTAAATCCAAACTGCTTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCCAAACTGCTAAATCAACTCCAAACTGCTAAATCAACTCCAAACTGCTAAATCAAACTCC	GFP-Xhof	7220	TCGAAAGGGTAATGGCCAGCAAAGAAA	11
7222 GGCCAAGGGTCTGAATGGGGCCGATAGT 7222 GGCCAAGGGTCTGAATGGGGCCGCATAGT 8417 GTTCCGAAGGGTCGAGGTCGAAGGAAGG 8418 GCGAAGGGTTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGG	GFP-Notr	6682	GGCCAAGGGTTTGTAGAGCTCATCCAT	12
6948 AAGCCATAGAGCCCGGGCCA 8417 GTTCCGAAGGGTCGACCTGCAGCTG 8418 CGGAACCAAGGGTCGACCTGCAGCAGG 8420 TAGGCCAAGGGTTGGCCATAGT 8419 GGCCTAAAGGGTGAATGGGCCCCATAGT 9304 GAAGGAGTAATACGACTCACTATAGGCCCCATAGT 9305 GTTCCGAAGGGCCCATGGTGCCTTTAGTGAGGCTCCTTTAGTGAGGCCTTTAGTGAGGCCTTTAGTGAGGCCTTTAGTGAGGCCCTTTAGTGAGGCTTTAGTTAG	BGHZ	7222	GGCCAAGGGTCTGAATGGGGCCGCATAGT	13
8417 GTTCCGAAGGGTCGAGCTGCAGCTG 8418 CGGAACAAGGGTTGGACCTGCAGGAGG 8420 TAGGCCAAGGGTTGTAGAGGTCATGC 8419 GGCCTAAAGGGTGATTGTAGGGCCCCATAGT 9304 GAAGGAGTAATACGACTCACTATAGGGAGCCACCATGGGCCCTTCGGAAC 9305 GTTCCGAAGGGCCCATGGTGGCTCCTATAGTGAGTCCTTC 9306 GAAGGAGTAATACGACTCACT 9306 GAAGGAGTAATACGACTCACT 9851 GAGCCTAAAGGGTCCCTTTAGTGAGGCCCTTTAGTGCCC 10632 GCGCGCAATTAACCCTCAAAGGGACCCTTTAGATCCCGCCTTTTACA 10632 GCGCGCAAGGGGACCATTTTCAATCCGCACCT 10770 TAGGCCAAGGGGACCATTTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTTCACCCAAGCTTGCCA 10772 TAGGCCAAGGGGACCATTGACACCAAGCTTGCTA	BGHr	6948	AAGCCATAGAGCCCGGGCCA	14
8418 CGGAACAAGGGATGGCCAGCAAGGAGAAG 8420 TAGGCCAAGGGTTGTAGAAGGAGAAG 8419 GGCCTAAAGGGTTGTAGT 9304 GAAGGAGTAATACGACTCACTATAGGAGCCACCATGGCACCTTCGGAAC 9305 GTTCCGAAGGGCCCATGGTGGCTCCCTTTAGTGGAGTCGTTTAGTCCCTTC 9308 GAAGGAGTAATACGACTCACT 9861 GAAGGAGTAATACGACTCACT 9862 GCCCGAATTAACCCTCACTAAGGGACCCTTTAGGCC 1062 GCGCGCAATTAACCCTCACTAAGGGACCCTTTAGGCC 10770 TAGGCCAAGGGGACCATTTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTTCACCCACGCT 10772 TAGGCCAAGGGGACCATTGACACCAACTGGTA	CMVr3	8417	GTTCCGAAGGGTCGAGGTCAACTTA	15
8420 TAGGCCAAGGGTTTGTAGAGCTCATCCATGC 8419 GGCCTAAAGGGTTGAATGGGGCCCATAGT 9304 GAAGGATAATACGACTCATATGGGAGCCACCATGGGCCCTTCGGAAC 9308 GAAGGAGTAATACGACTCACT 9308 GAAGGAGTAATACGACTCACT 9561 GGCCTAAAGGGCCCATGGTGGCTCCTTTAGTGAGGGCTTTAGTGGCC 1052 GCGCGAATTAACCCTCACTAAAGGGACCCTTTAGGC 10770 TAGGCCAAGGGGACCATTTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTTCAATCCGCACCT 10772 TAGGCCAAGGGGACCATTGACCAGACCAACTGGTA	GFPt3	8418	CGGAACAAGGGATGGCCAAGAAGGAAAG	16
8418 GGCCTAAAGGGTGAATGGGGCCGCATAGT 9304 GAAGGAGTAATACGACTCACTATAGGGAGCCACCATGGGCCCTTCGGAAC 9305 GTTCCGAAGGGCCCATGGTGTAATAGTGAGTCGTATAGTGAGTCGTTTC 9308 GAAGGATAATACGACTCACT 9561 GAGCCTAAAGGGTCCCTTTAGTGAGGGTTAATTGCGCC 10632 GCGCGCAATTAACCCTCACTAAAGGGACCCTTTAGGC 10632 CGGCAACAAGGGATGATAGATCCGCACCTTTACA 10770 TAGGCCAAGGGGACCATTTCACTCACCGCACCTT 10771 TAGGCCAAGGGGACCATTTCACCGCTTGCCA 10772 TAGGCCAAGGGGACCATTTCACCGCTTGCCA	GFPr3	8420		17
9304 GAAGGAGTAATACGACTCACTATAGGGAGCCACCATGGGCCTTCGGAAC 9305 GTTCCGAAGGGCCCATGGTGGCTCCCTATAGTGAGTCGTATTACTCCTTC 9308 GAAGGAGTAATACGACTCACT 9661 GGCCTAAAGGGTCCCTTTAGTGAGGGTTAATTGCGCC 10632 GCGCCAAAGGGTCCCTTTAGTGAGGGTTAATTGCGCC 10632 GCGCAACAAGGGACCATTAGTGAGACCGTTTACA 10770 TAGGCCAAGGGACCATTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTCACCCTTGCCA 10772 TAGGCCAAGGGGACCATTGACCCCAGGCGTGCCA	BGHR3	8419		18
m 9305 GFTCCGAAGGGCCCATGGTGGTCCCTATAGTGAGTCGTATTACTCCTTC 9308 GAAGGAGTAATACGACTCACT 9861 GAAGGAGTAATACGACTCACT m 9662 10632 GCGCGCAATTAACCCTCACTAAGGGACCCTTTAGGC 10770 TAGGCCAAGGGGACCATTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTCACACCAGGCGTTGCA 10772 TAGGCCAAGGGGACCATTGACACCAGACCAGTGATACCAACTGGTA	T7top	9304	1	19
9308 GAAGGAGTAATACGACTCACT 9661 GGCCTAAAGGGTCCCTTTAGTGAGGGTTAATTGCGCGC 10632 GCGCCAATTAACCCTCACTAAAGGGACCCTTTAGGC 10770 TAGGCCAAGGGACCATTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTCACCGCTTGCCA 10772 TAGGCCAAGGGGACCATTCACCAGACTGGTA	T7bottom	19305		20
9661 GGCCTAAAGGGTCCCTTTAGTGAGGGTTAATTGCGCGC 10632 GCGCAATTAACCCTCACTAAAGGGACCCTTTAGGCC 10632 CGGAACAAGGGATGATAGATCCCGTCGTTTTACA 10770 TAGGCCAAGGGGACCATTTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTTCACCGCTTGCCA 10771 TAGGCCAAGGGGAGCCACTTCACCGCTTGCCA	T7amp	9308	מונים מים ומים ואים ואים ומים ומים ומים ומים ומים ומים ומים ומ	21
m 8662 GCGCGCAATTAACOCTCACTAAAGGGACCCTTTAGGCC 10632 CGGAACAAGGGATGATAGATCCGGTGTTTTACA 10770 TAGGCCAAGGGGACCATTTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCATTTCACCGCTTGCCA 10771 TAGGCCAAGGGGACCATTCACCGCTTGCCA	T3top	9661		22
10632 CGGAACAAGGGATGATAGATCCGGTGTTTTACA 10770 TAGGCCAAGGGGACCATTTCAATCCGCACCT 10771 TAGGCCAAGGGGACCACTTCACCGCTTGCCA 10772 TAGGCCAAGGGTTTGACACCAAGGGTTTGACACCAACTGGTA	T3bottom	9662 .		23
10770 TAGGCCAAGGGGACCATTITCAATCCGCACCT 10771 TAGGCCAAGGGGAGCACTTCACCGCTTGCCA 10772 TAGGCCAAGGGTTTGACACCAGACCAACTGGTA	lacZi2	10632		24
10771 TAGGCCAAGGGGACTTCACCGCTTGCCA 10772 TAGGCCAAGGGTTTGACACCAGACCAACTGGTA	lacZ1k2	10770	27	25
10772 TAGGCCAAGGGTTTGACACCAGACTGGTA		10771		56
		10772		27
				8 0

FIGURE 92

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Mammalian Two-Hybrid		₹-	
	B-Gal activity 700000 700000		
	Sample # LacZ activ 1 240000 2 140000 3 1800000 4 1400000 5 54000 6 80000	9 42000	100

FIGURE 10

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B.

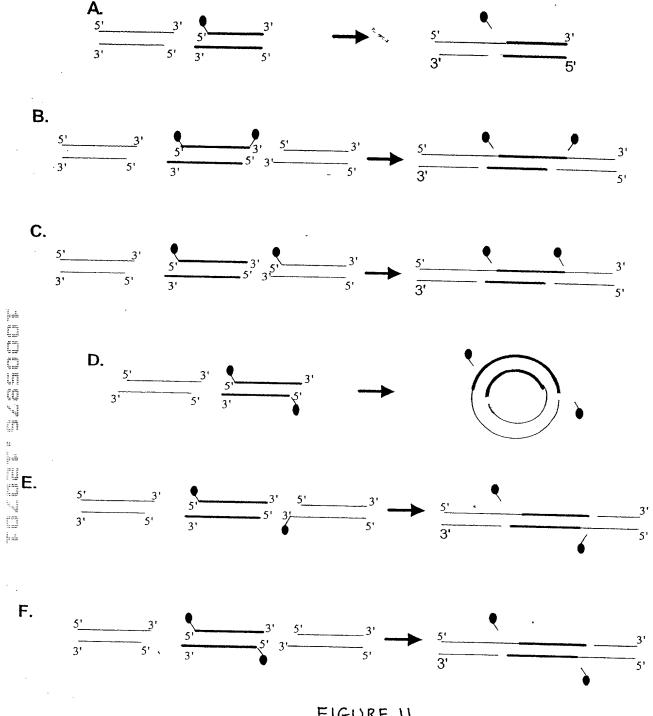


FIGURE 11

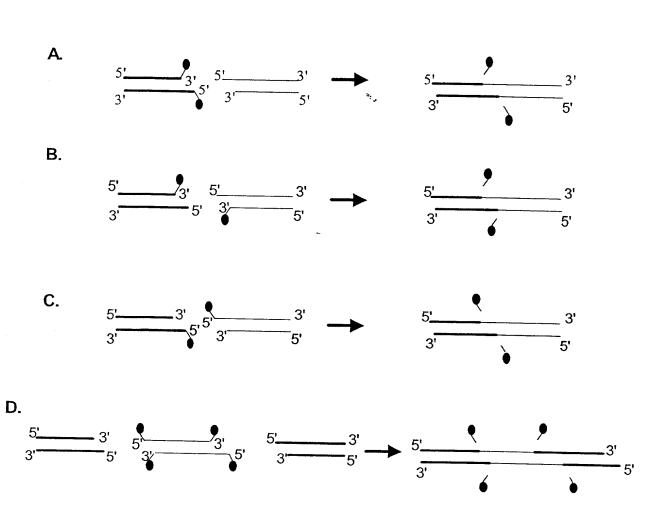


FIGURE 12

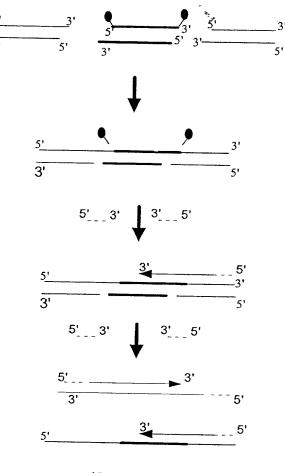
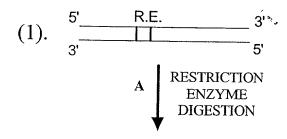
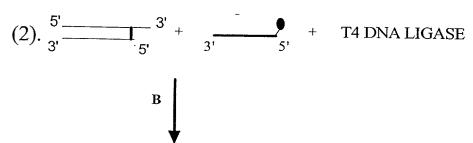
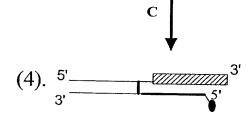


FIGURE 13









DS DNA
$$\frac{3'}{5'}$$
 + SSRNA $\frac{3'}{5'}$ $\frac{5'}{5'}$ $\frac{3'}{5'}$ $\frac{5'}{5'}$

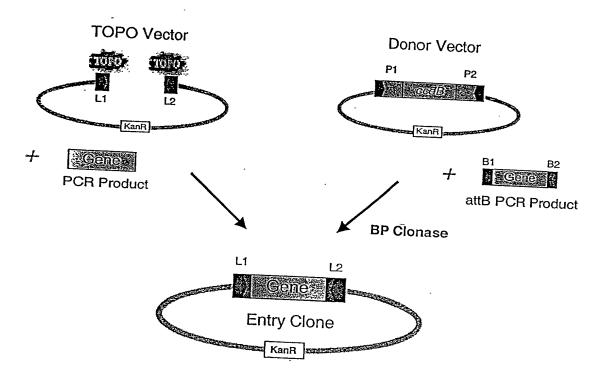


FIGURE 16

FIGURE 17

MCS for pcDNAGW-DT(sc) and pENTR-DT(sc) L Y K K A G S A A A TTG TAC AAA AAA GCA GGC TCC GCG GCC GCC GTA CTC GAG AAA GGG CGC GCC GAC CCA GCT TTC TTG TAC AAA GTG BsrG I AUU /B2 AUU /B2

FIGURE 18

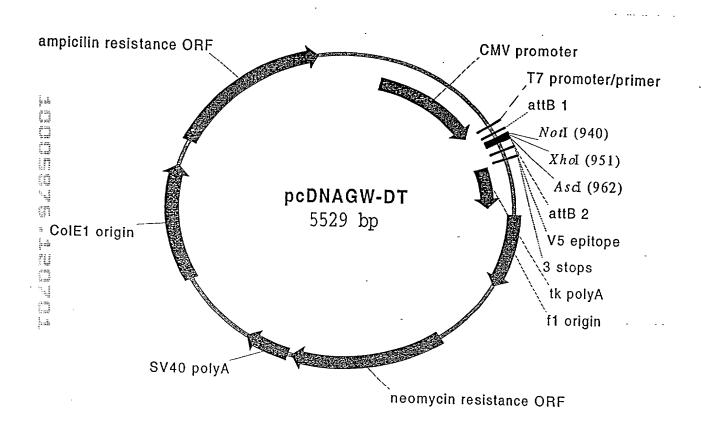


FIGURE 19

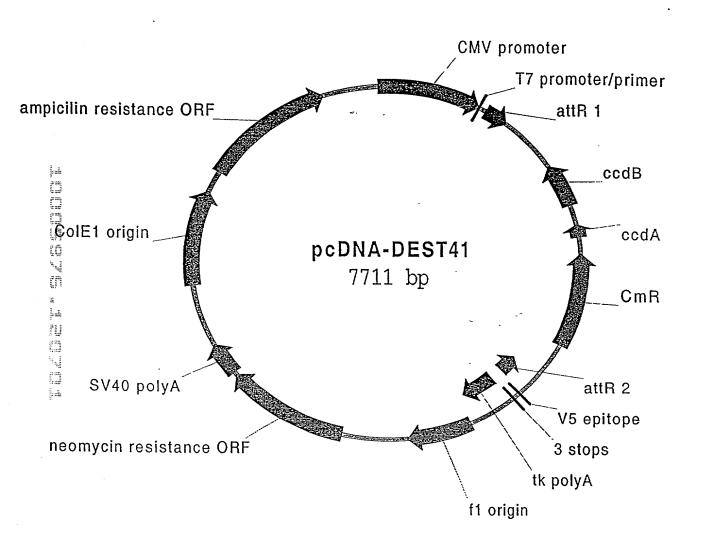


FIGURE 20

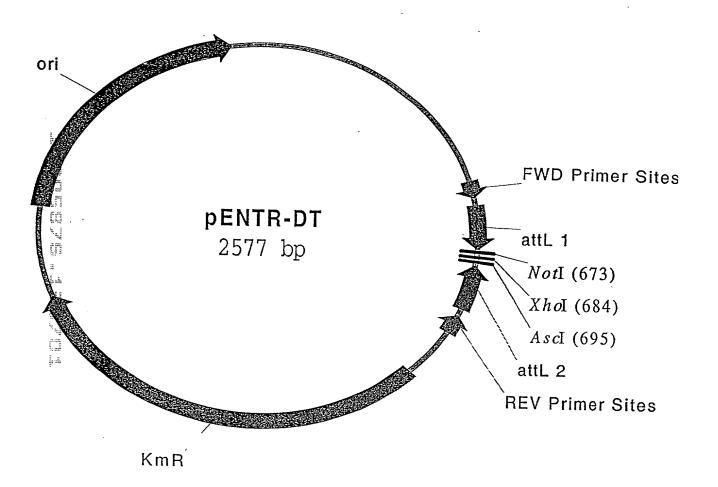


FIGURE 21

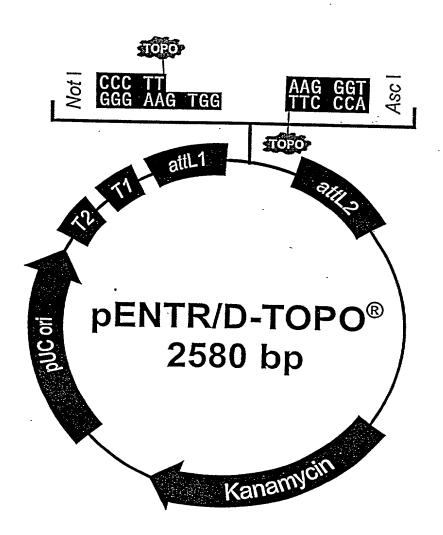


FIGURE 22A

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FIGURE 22B

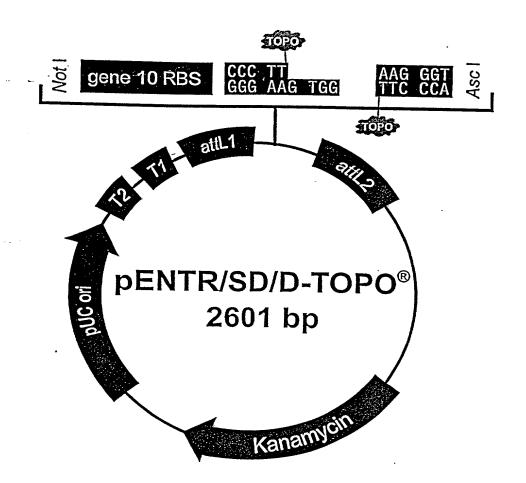


FIGURE 23A

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FIGURE 23B

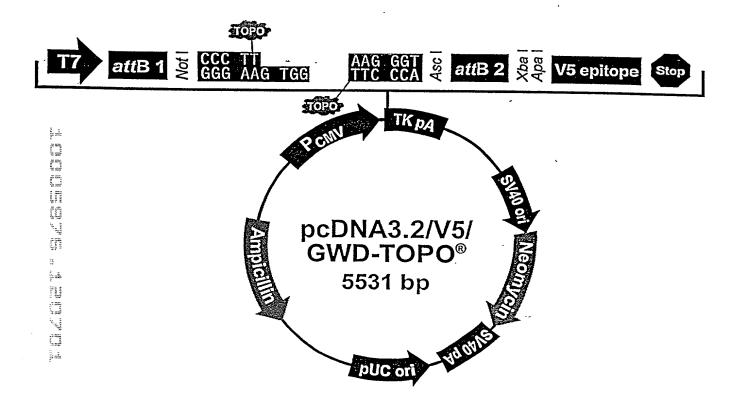


FIGURE 24A

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FIGURE 25A

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... TTG TAC AAA AAA GCA GGC TCC GCG GCC GCC TTG TTT AAC TTT AAG AAG GAG CCC TTC ACC ATG NNN NNN ... Comment of the Commen Not I G GCC GCC TTG TTT AAC TTT AAG AAG GAG CCC TTC ACCGACTATGTACAGITG Topo-D71 CGG AACAAA TTG AAA TTC TTC CTC GGG AAGTGG ļ. CTGATACATGIC Topo-D70 Topo-D72 ENTR-dTopo and pcDNAGW-dTopo: 5' end ... TTG TAC AAA AAA GCA G*GC TCC <u>GCG GCC GCC</u>* CCC TTC ACC **ATG NNN NNN ...** Secretary Vatt Billion Control of the Control of th Not I G GCC GCC CCCTTC ACCGACTATGTACAGTTG Topo-D73 CGG GGG AAGTGG CTGATACATGTC Topo-D70 Topo-D74 ENTRISD-dTopo, pENTR-dTopo, and pcDNAGW-dTopo: 3' end A \mathbf{F} \mathbf{L} К G G R D Y K ...NNN NNN AAG GGT GGG CGC GCC GAC CCA GCT TTC TTG TAC AAA GTG P.S. S. ORE . 1000 C GCG CCC ACC CTTGACATAGTACAGTTG Topo-D75 GGG TGG GAA CTGTATCATGTC Topo-D70 Topo-D76

pENTR/SD-dTopo: 5'end

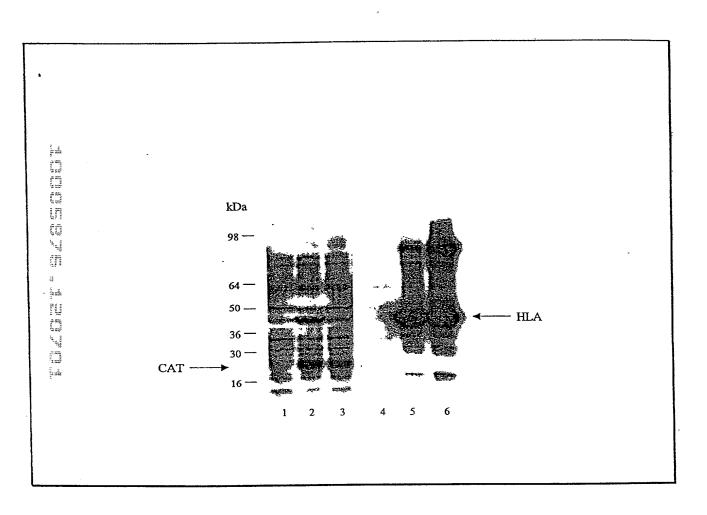


FIGURE 27

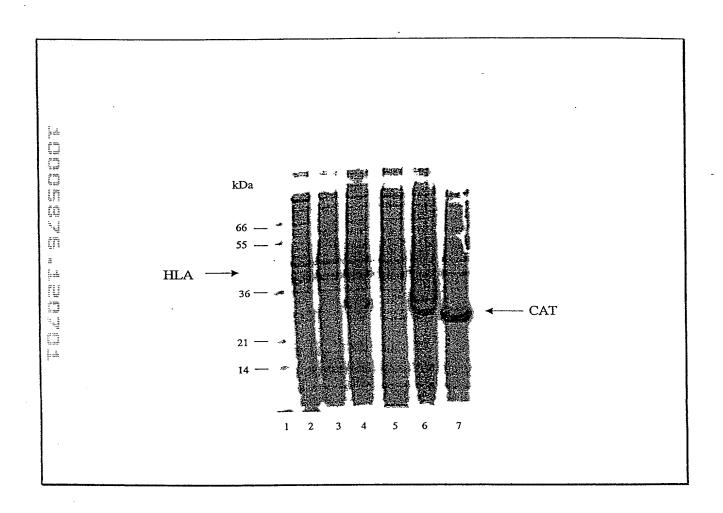


FIGURE 28

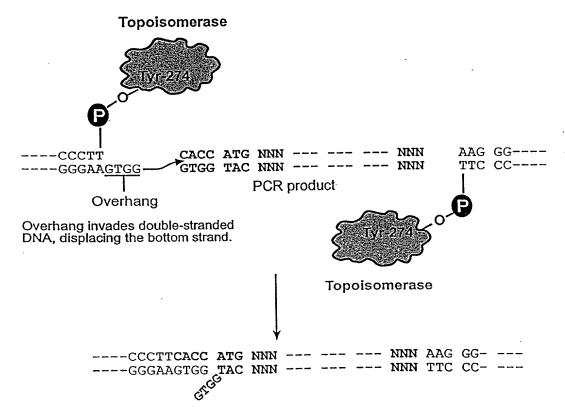
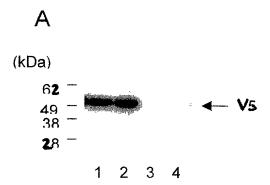
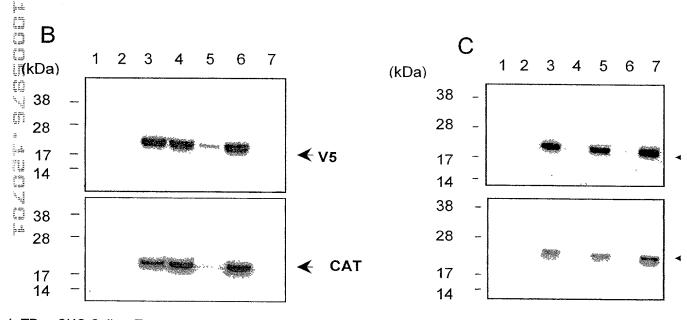


FIGURE 29



Lane 1: pCMVTetO/CAT/V5TKpA (without secondary PCR)+ Tet Lane 2: pCMVTetO/CAT/V5TKpA (with secondary PCR)+ Tet Lane 3: pCMVTetO/CAT/V5TKpA (with secondary PCR) - Tet Lane 4: pCMVTetO/CAT/V5TKpA (without secondary PCR)- Tet



Lane 1: TRex-CHO Cells + Tet Lane 2: without secondary PCR (with purified CAT) - Tet

Lane 3: without secondary PCR (with purified CAT)+ Tet Lane 4: without secondary PCR (with unpurified CAT) + Tet

Lane 5: without secondary PCR (with unpurified CAT) - Tet

Lane 6: with secondary PCR + Tet

Lane 7: with secondary PCR -Tet

Lane 1: TRex-293 Cells + Tet

Lane 2: without secondary PCR (with purified CAT) - Tet Lane 3: without secondary PCR (with purified CAT) + Tet

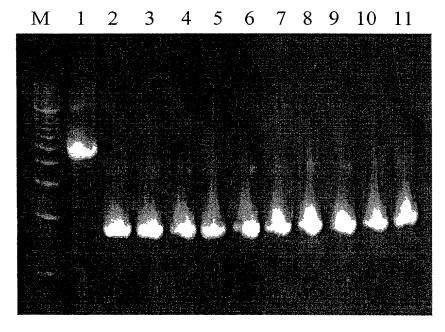
Lane 4: without secondary PCR (with unpurified CAT) - Teb

Lane 5: without secondary PCR (with unpurified CAT) + (etc.)

Lane 6: with secondary PCR - Tet

Lane 7: with secondary PCR + Tet

FIG. 30



Lane1: negative control; lanes 2-11: test clones; M: 500 bp marker

FIG. 31.

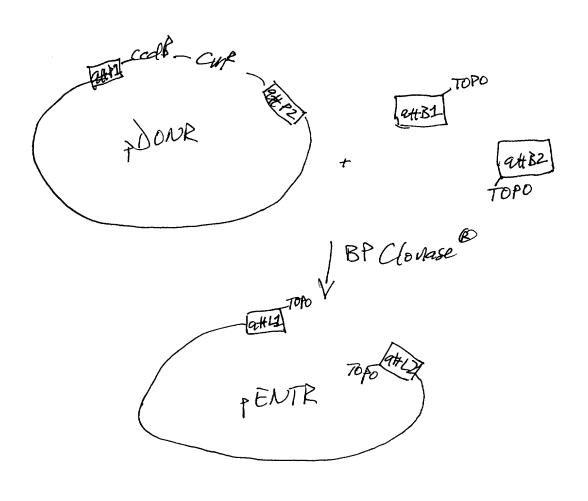
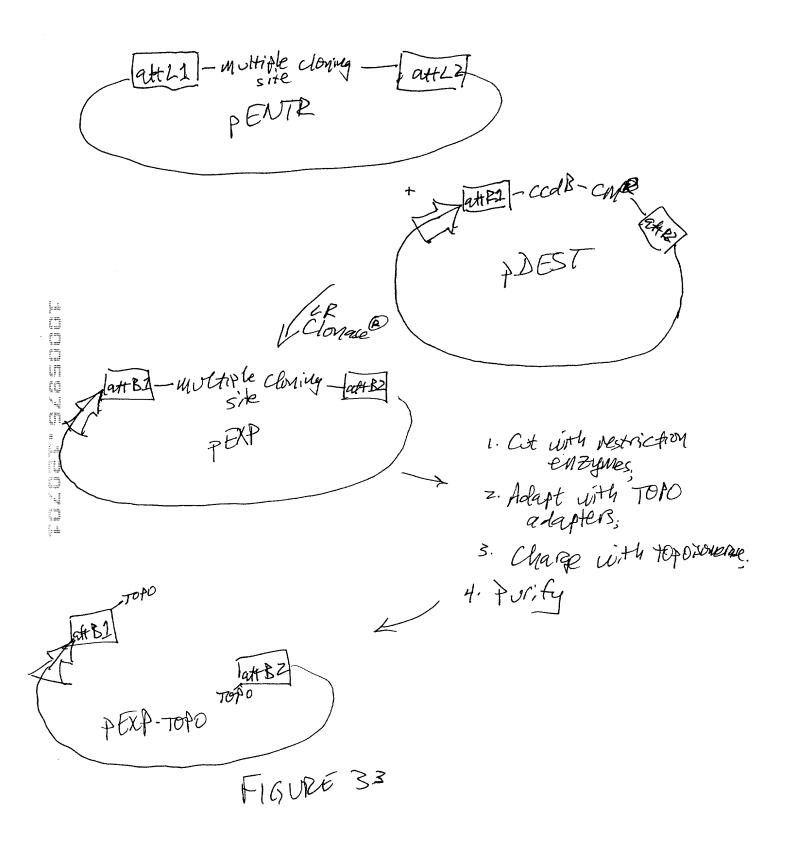


FIGURE 32



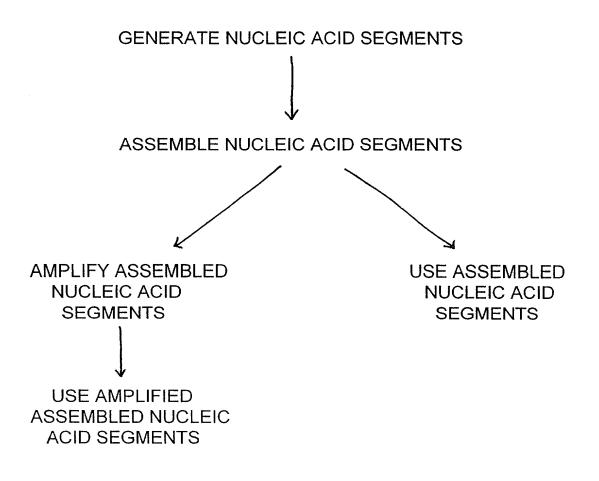


FIG. 34

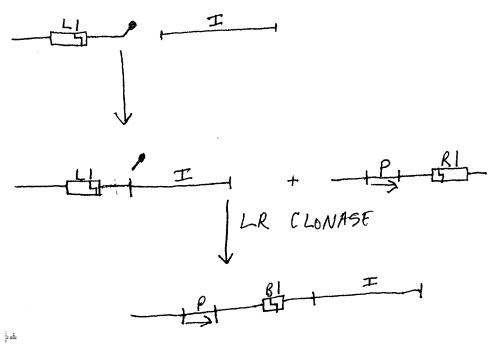


FIGURE 35

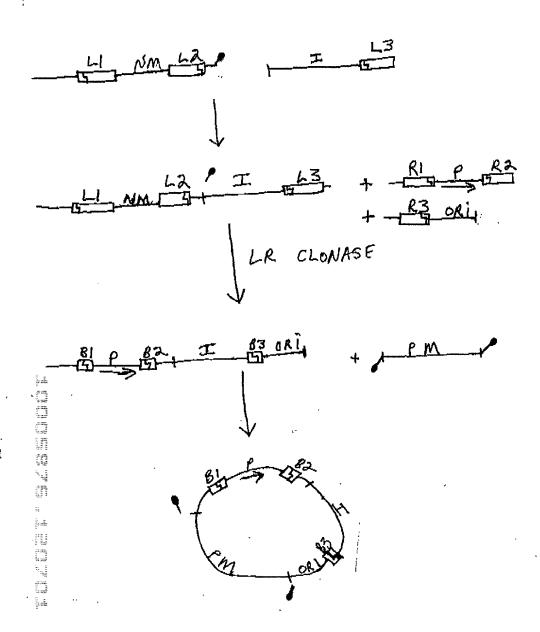
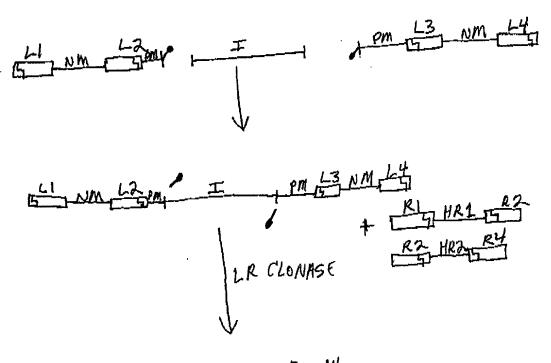


FIGURE 36



BI HRI BZFM # PMB3HRZ BY

FIGURE 37

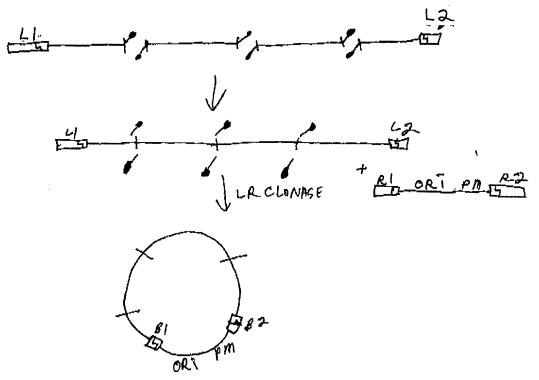


FIGURE 38

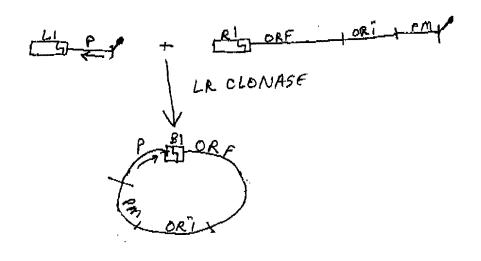
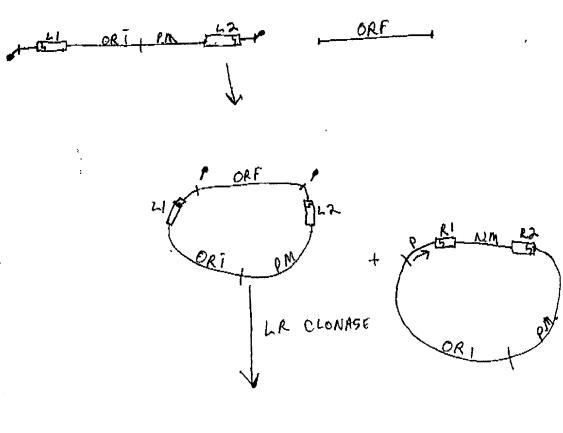


FIGURE 39



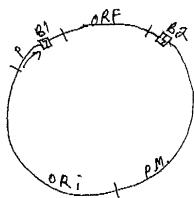


FIGURE 40